

Figure 10A-10C The representative prokaryotic phylogenetic tree in Newick format.

Figure 10A

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('Msr.barker'> Methanosarcina barkeri str. 227 DSM 1538' : 0.13236 , ('Msp.hungate'> Methanospirillum hungatei
str. JF1 DSM 864 (Ty' : 0.16948 ) : 0.24421 , ('Hf.volcani'> Haloferax volcanii str. DS-2 ATCC 29605 (Ty' : 0.03648
) : 0.09112 , ('cenv.SBAR16'> Santa Barbara Channel bacterioplankton DNA clone SBAR16' : 0.19448 ,
'<Tpl.acidop'> Thermoplasma acidophilum str. 122-1B2' : 0.22004 ) : 0.04224 ) : 0.10775 , ('Arg.fulgid'>
Archaeoglobus fulgidus str. VC-16 DSM 4304 (Ty' : 0.04075 ) : 0.05544 , ('Mb.formici'> Methanobacterium
formicicum DSM 1312' : 0.03067 , ('Mt.fervid'> Methanothermus fervidus' : 0.19624 ) : 0.01978 ) : 0.0947 ,
'<Tc.celer'> Thermococcus celer str. VU 13 DSM 2476 (Ty' : 0.00981 ) : 0.05532 , ('Mc.vanniel'> Methanococcus
vannielii str. EY33' : 0.02484 , ('Mc.jannase'> Methanococcus jannaschii str. JAL-1 DSM 2661 (Ty' : 0.1614 ) :
0.00857 ) : 0.02807 , ('Mpy.kandi1'> Methanopyrus kandleri str. av19 DSM 6324 (Ty' : 0.09845 ) : 0.02703 ,
('cenv.pJP27'> Mud Volcano area of Yellowstone NP ("Black Pool") hot spring DNA clone pJP27' : 0.06783 ,
('cenv.SBAR12'> Santa Barbara Channel bacterioplankton DNA clone SBAR12' : 0.1046 , ('cenv.pJP89'> Mud
Volcano area of Yellowstone NP ("Black Pool") hot spring DNA clone pJP89' : 0.28523 ) : 0.01132 ,
('<Tmf.penden'> Thermofilum pendens str. Hvv3 DSM 2475 (Ty' : 0.04404 , ('<Sul.acalida'> Sulfolobus
acidocaldarius str. 98-3 ATCC 33909 (Ty' : 0.04024 , ('<Thp.tenax'> Thermoproteus tenax' : 0.15875 ) : 0.02106 ) :
0.09273 ) : 0.20883 ) : 0.03789 ) : 0.31178 , ('<Aqu.pyroph'> Aquifex pyrophilus str. Kof5a' : 0.20649 ,
('<Tt.maritum'> Thermotoga maritima str. MSB8 DSM 3109 (Ty' : 0.01001 , ('<Fer.island'> Fervidobacterium
islandicum str. H-21 DSM 5733 (Ty' : 0.16351 ) : 0.23062 , (('<Mei.ruber4'> Meiothermus ruber str. Loginova 21
ATCC 35948 (Ty' : 0.14908 , '<D.radiodur'> Deinococcus radiodurans ATCC 35073' : 0.19907 ) : 0.08298 ,
'<C.fk.aurant'> Chloroflexus aurantiacus str. J-10-II ATCC 29366 (Ty' : 0.1976 , '<Tmc.rosenum'> Thermomicrobium
roseum ATCC 27502 (Ty' : 0.36297 ) : 0.11213 ) : 0.01165 , (((((((((((('<Acp.lajida'> Achaetoplasma laidlawii str.
JAI' : 0.11002 , '<C.ramosum'> Clostridium ramosum str. 113-I ATCC 25582 (Ty' : 0.30774 ) : 0.00736 ,
'<M.capricol'> Mycoplasma capricolum ATCC 27343 (Ty' : 0.38452 ) : 0.10528 , '<Stc.therm3'>
Streptococcus thermophilus DSM 20617 (Ty' : 0.05073 ) : 0.15065 , '<Eco.faecal'> Enterococcus faecalis' : 0.0306 ) :
0.01738 , ('<L.casei'> Lactobacillus casei subsp. casei ATCC 393 (Ty' : 0.13937 , '<L.delbruck'> Lactobacillus
delbrueckii subsp. delbrueckii str. Calvert ATCC 9649 (Ty' : 0.04809 ) : 0.01852 ) : 0.02217 , '<Lis.monoc3'>
Listeria monocytogenes' : 0.02418 ) : 0.0404 , '<B.cereus4'> Bacillus cereus IAM 12605 (Ty' : 0.06989 ) : 0.0034 ,
'<B.subtilis'> Bacillus subtilis str. 168' : 0.05051 , '<B.stearoth'> Bacillus stearothermophilus NCD0 1768 (Ty' :
0.05959 ) : 0.0075 ) : 0.12658 , '<Eub.barker'> Eubacterium barkeri ATCC 25849 (Ty' : 0.28781 ) : 0.0097 ,
('<C.quericco'> Clostridium quericolum ATCC 25974 (Ty' : 0.13519 , '<Hel.chlor2'> Hellobacterium chlorum
ATCC 35205 (Ty' : 0.1075 ) : 0.01024 ) : 0.01183 , ('<Fus.nuclea'> Fusobacterium nucleatum subsp. nucleatum
ATCC 25586 (Ty' : 0.08593 , ('<Stm.ambofa'> Streptomyces ambofaciens' : 0.06051 , ('<Cor.xerosi'>
Corynebacterium xerosis ATCC 373 (Ty' : 0.10315 , ('<Bif.bifidu'> Bifidobacterium bifidum ATCC 29521 (Ty' :
0.29842 , '<Arb.globif'> Arthrobacter globiformis str. 168 DSM 20124 (Ty' : 0.12957 ) : 0.06797 ) : 0.00748 ) :
Docket 010AUS; USSN 10/057,270; Figure 10A-10C The representative prokaryotic phylogenetic tree in Newick
format.

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Figure 10B

0.3137) : 0.01738) : 0.00511, ('<C.leptum> Clostridium leptum ATCC 29065 (TY : 0.16126, ('<C.butyric4> Clostridium butyricum str. E.V1.3.6.1 NCIMB 8082' : 0.06037, '<C.pasteur> Clostridium pasteurianum ATCC 6013 (TY : 0.07626) : 0.38023) : 0.02432) : 0.01262, (((((((('<Rub.gelati2> Rubrivivax gelatinosus str. ATH 2.2.1 ATCC 17011 (TY : 0.07169, '<Spr.voluta> Spirillum volutans ATCC 19554 (TY : 0.06661) : 0.00462, '<Rey.purpur> Rhodocyclus purpureus str. 6770 DSM 168 (TY : 0.04015) : 0.02165, '<Nis.gonor1> Neisseria gonorrhoeae str. B 5025 NCTC 8375 (TY : 0.19789) : 0.01431, '<Ste.maltop> Sienotrophomonas maltophilia ATCC 13637 (TY : 0.24098) : 0.02299, '<E.coli> Escherichia coli [gene=rrnB operon]' : 0.05825, '<Ps.aerugi3> Pseudomonas aeruginosa DSM 50071 (TY : 0.63646) : 0.03524) : 0.04488, '<Alm.vinosu> Allochrocatium vinosum ATCC 17899 (TY : 0.0233) : 0.04869, '<Hrh.halch2> Halorhodospira halochloris str. A ATCC 35916 (TY : 0.05948) : 0.08019, ('<R.rubrum3> Rhodospirillum rubrum str. ATH 1.1.1: S.1 ATCC 11170 (TY : 0.04904, '<Azs.bras12> Azospirillum brasilense str. Sp 7 NCIMB 11860 (TY : 0.3086) : 0.01343, ('<Ric.prowaz> Rickettsia prowazekii str. Breinl ATCC VR-142 (t (alpha purple bacterium)' : 0.1406, '<Spg.capsul> Spingomonas capsulata ATCC 14666 (TY : 0.13872) : 0.02068, ('<Rhb.legum8> Rhizobium leguminosarum IAM 12609 (TY : 0.01576, ('<Bdr.japoni> Bradyrhizobium japonicum LMG 6138 (TY : 0.05736, '<Rm.vanniel> Rhodocyclus vannielii str. EY33 ATCC 51194' : 0.093) : 0.04263) : 0.00617) : 0.03466) : 0.06772) : 0.00546, ('<Myx.xanthu> Myxococcus xanthus str. DK1622' : 0.11263, '<Dsb.postga> Desulfobacter postgatei str. 2 ac 9 DSM 2034 (TY : 0.19098) : 0.01154, ('<Dsv.desulf> Desulfovibrio desulfuricans subsp. desulfuricans ATCC 27774' : 0.01563, ('<Bde.siolpi> Bdellovibrio stolpii str. UKi2 ATCC 27052 (TY : 0.05967, ('<Cam.jejun5> Campylobacter jejuni subsp. jejuni str. TGH 9011 ATCC 43431' : 0.01753, ('<Wln.succi2> Wolinella succinogenes str. 602W (FDC) ATCC 29543 (TY : 0.05551, '<Hlb.pylor6> Helicobacter pylori ATCC 43504 (TY : 0.02351) : 0.18884) : 1.11671) : 0.18947) : 0.01602) : 0.15633) : 0.01513, (((((((('<Trp.pallid> Treponema pallidum str. Nichols' : 0.14543, '<Spi.sienos> Spirochaeta stenostrepta str. Z1 ATCC 25083 (TY : 0.03623) : 0.03698, '<Bor.burgdo> Borrelia burgdorferi str. B31 ATCC 35210 (TY : 0.3604) : 0.0859, '<Spi.halopi> Spirochaeta halophila str. RS1 ATCC 29478 (TY : 0.02473) : 0.01206, '<Brs.hydody> Brachyspira hyodysenteriae str. B204 ATCC 31212' : 0.43546) : 0.04129, ('<Lpn.illini> Leptonema illini str. 3055' : 0.07041, '<Lps.interK> Leptospira interrogans str. Kennewicki, serovar pomona' : 0.16902) : 0.05013) : 0.01817, ('<Fib.suc585> Fibrobacter succinogenes subsp. succinogenes str. S85 ATCC 19169 (TY : 0.23142, '<Acbt.capsl> Acidobacterium capsulatum str. 161' : 0.21099) : 0.03073) : 0.0094, (((((((('<Syn.6301> Synechococcus sp. PCC 6301' : 0.12285, '<Nost.muscr> Nostoc muscorum PCC 7120' : 0.06977) : 0.01225, '<Zea.mays_C> Zea mays (maize; corn; Indian corn) -- chloroplast' : 0.145, '<Olst.hnt_C> Olisthodiscus luteus (stramenopile) -- chloroplast' : 0.3525) : 0.09491) : 0.012, '<Glb.viola> Gloeobacter violaceus PCC 7421' : 0.07279) : 0.01171, ('<env.MC18> Mount Coot-tha region (Brisbane, Australia) 5-10cm depth soil DNA clone MC 18' : 0.01409, ('<Chd.psita> Chlamydomonas reinhardtii str. 6BC ATCC VR-125 (TY : 0.36004, '<Pir.staley> Pirellula staleyi ATCC 27377' : 0.34247) : 0.25993) : 0.1121) : 0.03258, ('<Chl.limico> Chlorobium limicola str. 8327' : 0.1389, ('<Tam.lapsun> Thermoanaerobium lapsun ATCC Docket 010AUS; USSN 10/057,270; Figure 10A-10C The representative prokaryotic phylogenetic tree in Newick format.

43542 (T)' : 0.0332 , ('<Flx.litora> Flexibacter litoralis str. Lewin SIO-4 ATCC 23117 (T)' : 0.01576 , ('<Cy.hutchin> Cytophaga hutchinsonii str. D465 (P.H.A. Sneath) ATCC 33406 (T)' : 0.0073 , ('<Prb.diffu>

Figure 10C

Persicobacter diffuens str. Lewin LIM-1 ATCC 23140' : 0.00585 , ('<Sap.grandi> Saprospira grandis ATCC 23119 (T)' : 0.02768 , ('<Flx.canada> Flexibacter canadensis ATCC 29591 (T)' : 0.03254 , ('<Bac.fragil> Bacteroides fragilis ATCC 25285 (T)' : 0.04826 , '<Prv.rumcol> Prevotella ruminicola subsp. ruminicola ATCC 19189 (T)' : 0.20539) : 0.02821 , ('<Cy.lytica> Cytophaga lytica str. LIM-21 ATCC 23178 (T)' : 0.14365 , '<Emb.brevi2> Empedobacter brevis ATCC 14234' : 0.0913) : 0.35994) : 0.12199) : 0.33291) : 0.47588) : 0.14622) : 0.18424) : 0.08878) : 0.30465) : 0.05104) : 0.00825) : 0.02261) : 0.00329) : 0.56238) : 0.52312) : 0.05444) : 0.31178) ; **Docket 010AUS; USSN 10/057,270; Figure 10A-10C** The representative prokaryotic phylogenetic tree in Newick format.